Figure 1. Nucleotide and amino acid sequences (SEQ ID Nos: 1 and 2) of the *C. pneumoniae* 60 kDa cysteine rich membrane protein

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ttgatcaggt agttaggaga tgaattaatt cctgactacc ttaattcaga taataaaccc 60

aaatgttgag ggtaagagtt tacaaaacat tctacccgat ggcagaagaa aaaaataaac 120

atgcgatagg agatccct atg tcc aaa ctc atc aga cga gta gtt acg gtc   171
                    Met Ser Lys Leu Ile Arg Arg Val Val Thr Val
                      1               5                  10

ctt gcg cta acg agt atg gcg agt tgc ttt gcc agc ggg ggt ata gag   219
Leu Ala Leu Thr Ser Met Ala Ser Cys Phe Ala Ser Gly Gly Ile Glu
             15                  20                  25

gcc gct gta gca gag tct ctg att act aag atc gtc gct agt gcg gaa   267
Ala Ala Val Ala Glu Ser Leu Ile Thr Lys Ile Val Ala Ser Ala Glu
         30                  35                  40

aca aag cca gca cct gtt cct atg aca gcg aag aag gtt aga ctt gtc   315
Thr Lys Pro Ala Pro Val Pro Met Thr Ala Lys Lys Val Arg Leu Val
     45                  50                  55

cgt aga aat aaa caa cca gtt gaa caa aaa agc cgt ggt gct ttt tgt   363
Arg Arg Asn Lys Gln Pro Val Glu Gln Lys Ser Arg Gly Ala Phe Cys
 60                  65                  70                  75

gat aaa gaa ttt tat ccc tgt gaa gag gga cga tgt caa cct gta gag   411
Asp Lys Glu Phe Tyr Pro Cys Glu Glu Gly Arg Cys Gln Pro Val Glu
                 80                  85                  90

gct cag caa gag tct tgc tac gga aga ttg tat tct gta aaa gta aac   459
Ala Gln Gln Glu Ser Cys Tyr Gly Arg Leu Tyr Ser Val Lys Val Asn
             95                 100                 105

gat gat tgc aac gta gaa att tgc cag tcc gtt cca gaa tac gct act   507
Asp Asp Cys Asn Val Glu Ile Cys Gln Ser Val Pro Glu Tyr Ala Thr
        110                 115                 120

gta gga tct cct tac cct att gaa atc ctt gct ata ggc aaa aaa gat   555
Val Gly Ser Pro Tyr Pro Ile Glu Ile Leu Ala Ile Gly Lys Lys Asp
    125                 130                 135

tgt gtt gat gtt gtg att aca caa cag cta cct tgc gaa gct gaa ttc   603
Cys Val Asp Val Val Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe
140                 145                 150                 155

gta agc agt gat cca gaa aca act cct aca agt gat ggg aaa tta gtc   651
Val Ser Ser Asp Pro Glu Thr Thr Pro Thr Ser Asp Gly Lys Leu Val
                160                 165                 170

tgg aaa atc gat cgc ctg ggt gca gga gat aaa tgc aaa att act gta   699
Trp Lys Ile Asp Arg Leu Gly Ala Gly Asp Lys Cys Lys Ile Thr Val
            175                 180                 185
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Figure 1 (cont'd)

tgg gta aaa cct ctt aaa gaa ggt tgc tgc ttc aca gct gct act gta 747
Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe Thr Ala Ala Thr Val
190 195 200

tgt gct tgc cca gag ctc cgt tct tat act aaa tgc ggt caa cca gcc 795
Cys Ala Cys Pro Glu Leu Arg Ser Tyr Thr Lys Cys Gly Gln Pro Ala
205 210 215

att tgt att aag caa gaa gga cct gac tgt gct tgc cta aga tgc cct 843
Ile Cys Ile Lys Gln Glu Gly Pro Asp Cys Ala Cys Leu Arg Cys Pro
220 225 230 235

gta tgc tac aaa atc gaa gta gtg aac aca gga tct gct att gcc cgt 891
Val Cys Tyr Lys Ile Glu Val Val Asn Thr Gly Ser Ala Ile Ala Arg
240 245 250

aac gta act gta gat aat cct gtt ccc gat ggc tat tct cat gca tct 939
Asn Val Thr Val Asp Asn Pro Val Pro Asp Gly Tyr Ser His Ala Ser
255 260 265

ggt caa aga gtt ctc tct ttt aac tta gga gac atg aga cct ggc gat 987
Gly Gln Arg Val Leu Ser Phe Asn Leu Gly Asp Met Arg Pro Gly Asp
270 275 280

aaa aag gta ttt aca gtt gag ttc tgc cct caa aga aga ggt caa atc 1035
Lys Lys Val Phe Thr Val Glu Phe Cys Pro Gln Arg Arg Gly Gln Ile
285 290 295

act aac gtt gct act gta act tac tgc ggt gga cac aaa tgt tct gca 1083
Thr Asn Val Ala Thr Val Thr Tyr Cys Gly Gly His Lys Cys Ser Ala
300 305 310 315

aat gta act aca gtt gtt aat gag cct tgt gta caa gta aat atc tct 1131
Asn Val Thr Thr Val Val Asn Glu Pro Cys Val Gln Val Asn Ile Ser
320 325 330

ggt gct gat tgg tct tac gta tgt aaa cct gtg gag tac tct atc tca 1179
Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val Glu Tyr Ser Ile Ser
335 340 345

gta tcg aat cct gga gac ttg gtt ctt cat gat gtc gtg atc caa gat 1227
Val Ser Asn Pro Gly Asp Leu Val Leu His Asp Val Val Ile Gln Asp
350 355 360

aca ctc cct tct ggt gtt aca gta ctc gaa gct cct ggt gga gag atc 1275
Thr Leu Pro Ser Gly Val Thr Val Leu Glu Ala Pro Gly Gly Glu Ile
365 370 375

tgc tgt aat aaa gtt gtt tgg cgt att aaa gaa atg tgc cca gga gaa 1323
Cys Cys Asn Lys Val Val Trp Arg Ile Lys Glu Met Cys Pro Gly Glu
380 385 390 395

acc ctc cag ttt aaa ctt gta gtg aaa gct caa gtt cct gga aga ttc 1371
Thr Leu Gln Phe Lys Leu Val Val Lys Ala Gln Val Pro Gly Arg Phe
400 405 410

aca aat caa gtt gca gta act agt gag tct aac tgc gga aca tgt aca 1419
Thr Asn Gln Val Ala Val Thr Ser Glu Ser Asn Cys Gly Thr Cys Thr
415 420 425

Figure 1 (cont'd)

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tct tgc gca gaa aca aca aca cat tgg aaa ggt ctt gca gct acc cat   1467
Ser Cys Ala Glu Thr Thr Thr His Trp Lys Gly Leu Ala Ala Thr His
        430                 435                 440

atg tgc gta tta gac aca aat gat cct atc tgt gta gga gaa aat act   1515
Met Cys Val Leu Asp Thr Asn Asp Pro Ile Cys Val Gly Glu Asn Thr
    445                 450                 455

gtc tat cgt atc tgt gta act aac cgt ggt tct gct gaa gat act aac   1563
Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser Ala Glu Asp Thr Asn
460                 465                 470                 475

gta tct tta atc ttg aag ttc tca aaa gaa ctt cag cca ata gct tct   1611
Val Ser Leu Ile Leu Lys Phe Ser Lys Glu Leu Gln Pro Ile Ala Ser
                480                 485                 490

tca ggt cca act aaa gga acg att tca ggt aat acc gtt gtt ttc gac   1659
Ser Gly Pro Thr Lys Gly Thr Ile Ser Gly Asn Thr Val Val Phe Asp
            495                 500                 505

gct tta cct aaa ctc ggt tct aag gaa tct gta gag ttt tct gtt acc   1707
Ala Leu Pro Lys Leu Gly Ser Lys Glu Ser Val Glu Phe Ser Val Thr
        510                 515                 520

ttg aaa ggt att gct ccc gga gat gct cgc ggc gaa gct att ctt tct   1755
Leu Lys Gly Ile Ala Pro Gly Asp Ala Arg Gly Glu Ala Ile Leu Ser
    525                 530                 535

tct gat aca ctg act tca cca gta tca gac aca gaa aat acc cac gtg   1803
Ser Asp Thr Leu Thr Ser Pro Val Ser Asp Thr Glu Asn Thr His Val
540                 545                 550                 555

tat taa attctaagga attatcctaa agcagagcga tattccgctc tgctttagga   1859
Tyr

tagctttcaa agaagtaccg ctttagtacc ttacgtacta aagcggtttt tttgttttat 1919

aagctcttca atccaatcgt agagtttctt aatcaaagat attatttaag tttctgaaat 1979

cctaagattt attttaaaag cccatctttt taggtatgta attaaaattt ttaattaagc 2039

ttttcctagt gtaacctgct tctttaggaa ctacactagg agaacggtat gtcatcaaat 2099

ctacatcccg ta                                                     2111
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Figure 2: Restriction enzyme analysis of the the *C. pneumoniae* 60 kDa cysteine rich membrane protein.

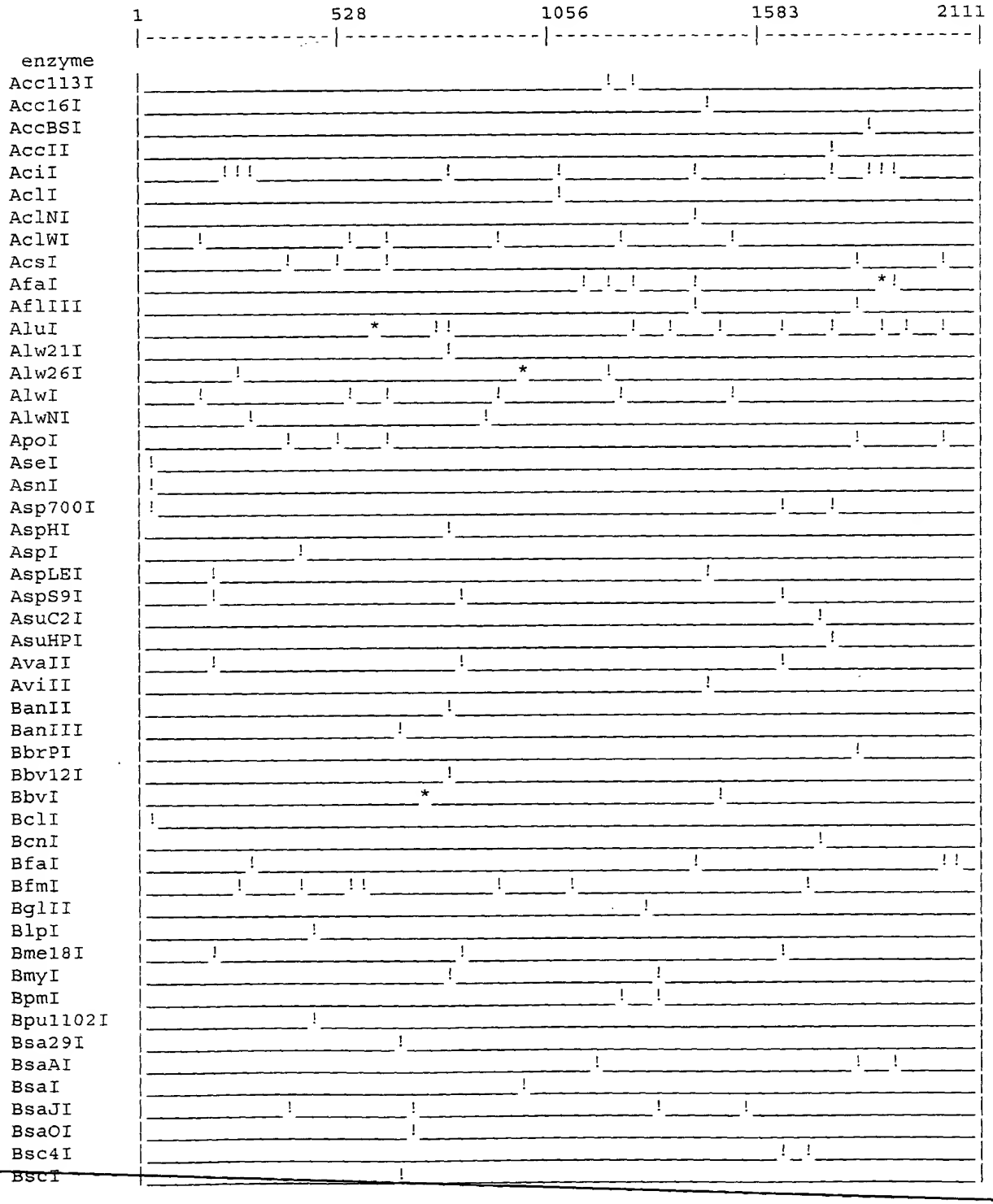


Figure 2 (cont'd)

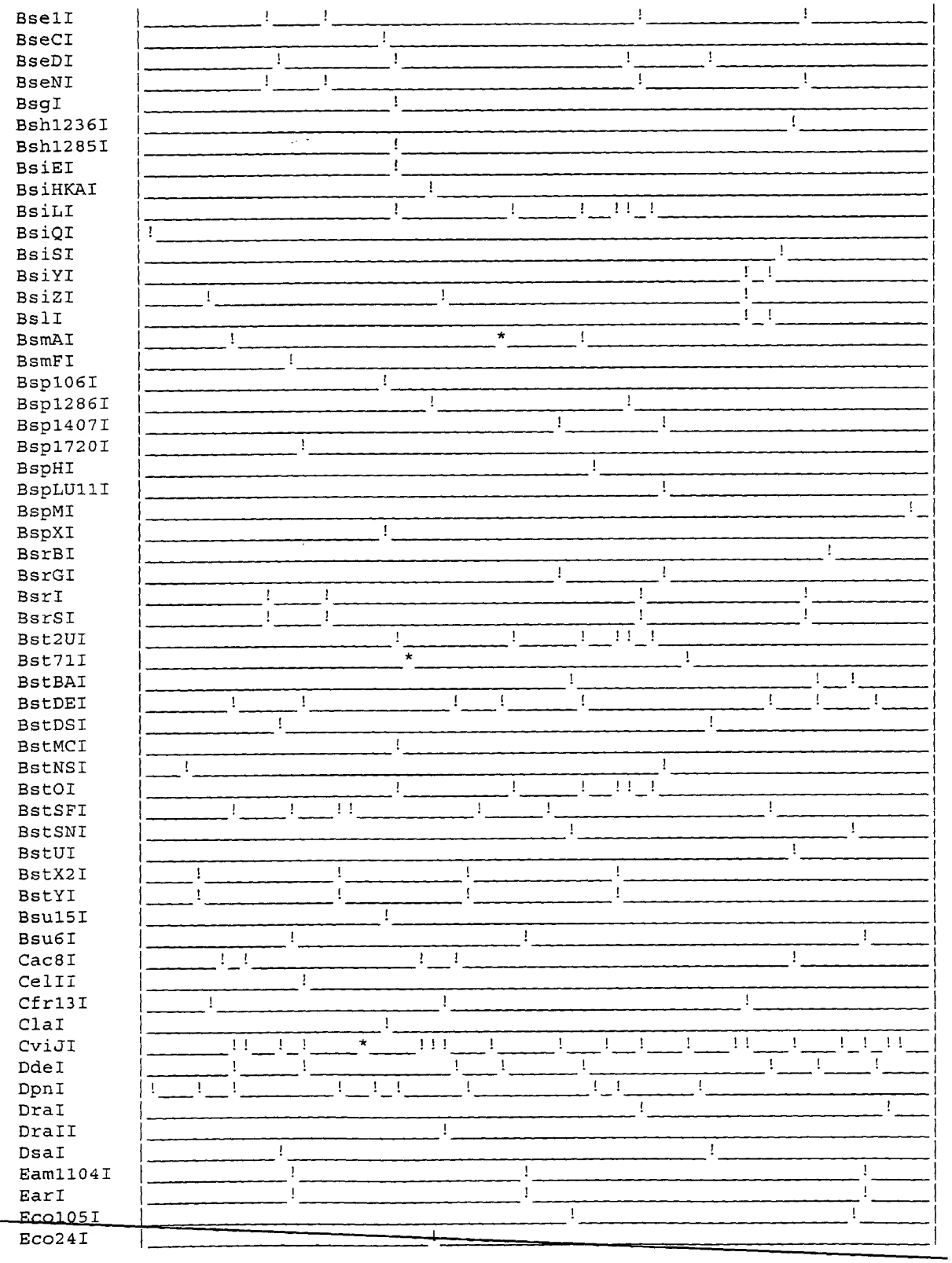


Figure 2 (cont'd)

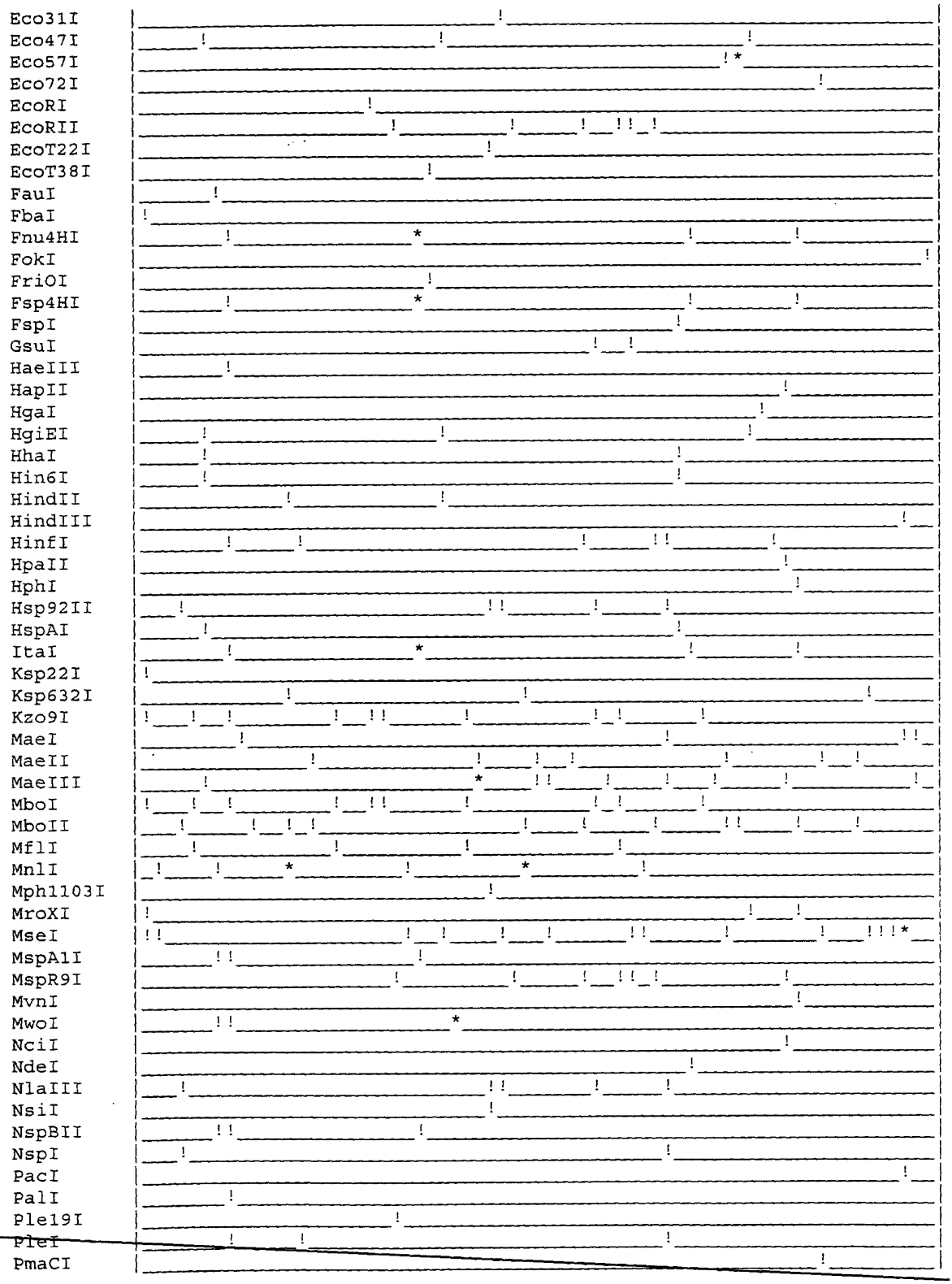
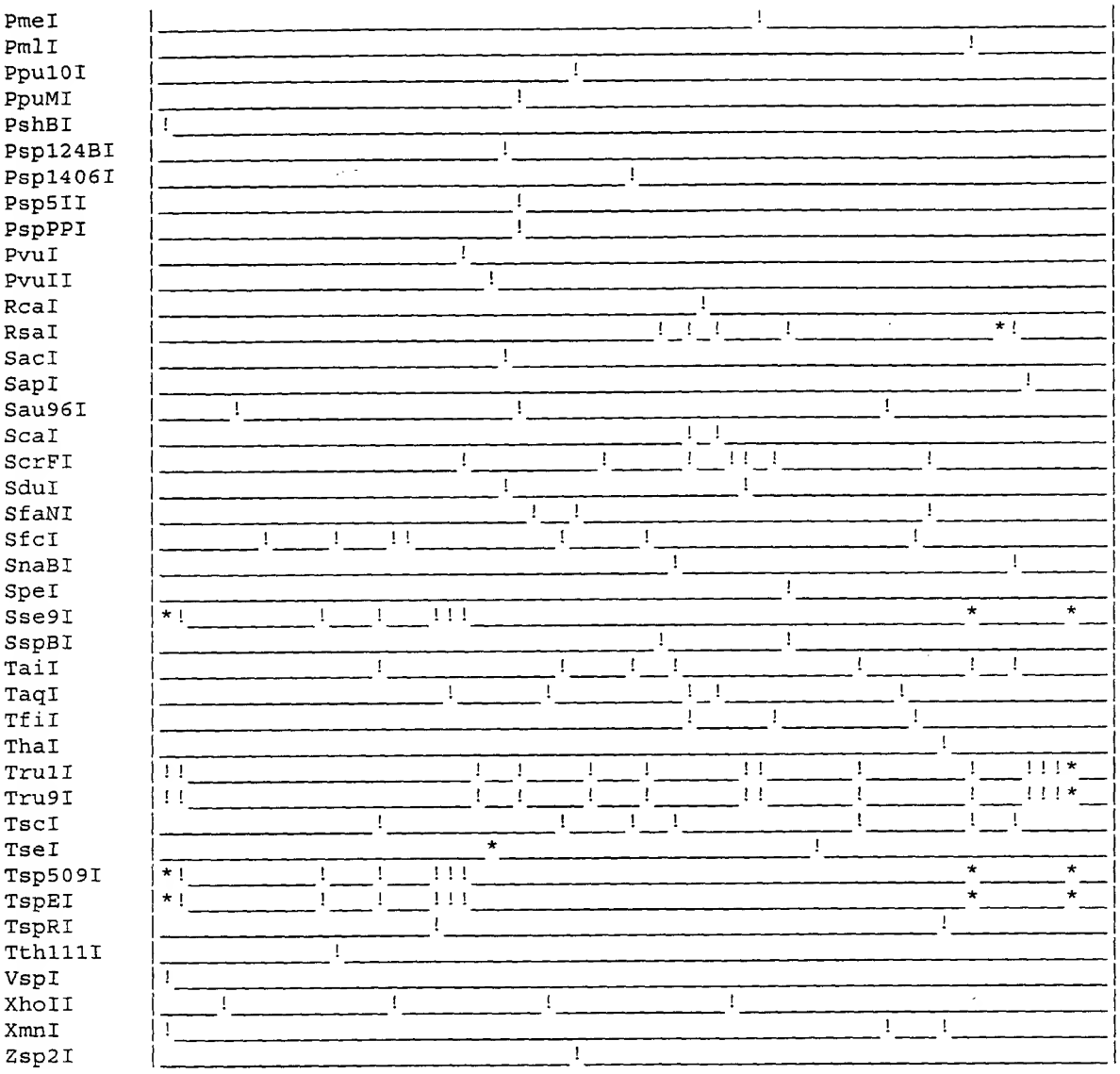


Figure 2 (cont'd)



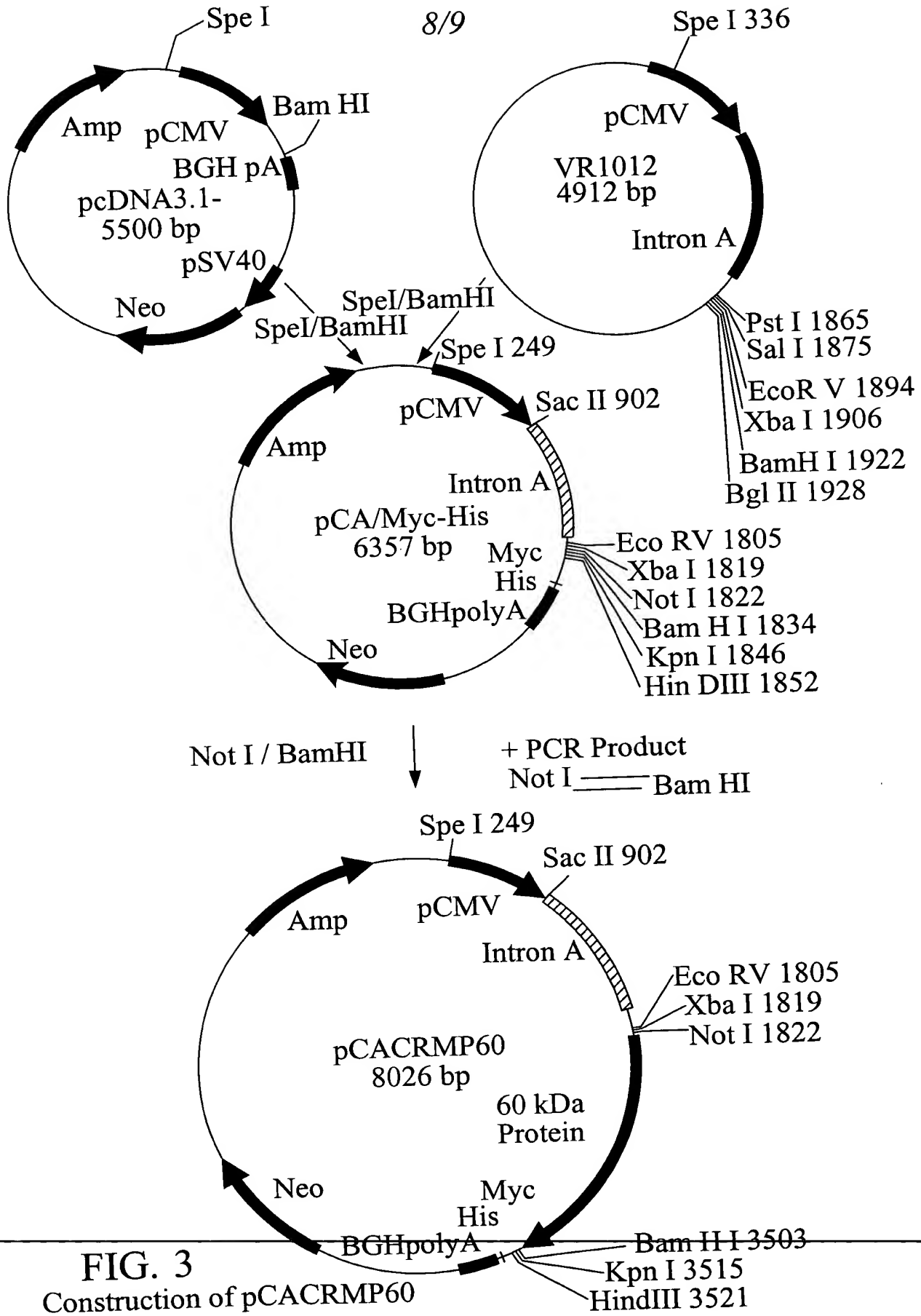


FIG. 3
Construction of pCACRMP60

Figure 4: Protective efficacy of DNA immunization with pCACRMP60 against intranasal challenge of *C. pneumoniae*